Amendments To The Specification

Please replace paragraph [0035] from US 2007/00506054 A1 with the following amended paragraph:

[0035] FIG. 4 shows (A) homozygosity for the nonsense mutation (AAA→TAA) in sap^{ta222a} dmd exon 4 segregated exclusively with the sap phenotype. (B) Rooted tree showing dystrophin and utrophin proteins in vertebrates. The tree is rooted using *Drosophila melanogaster* dystrophin. The numbers represent the percentage of 1000 bootstrap trials that support the branch. DYS, dystrophin; UTRO, utrophin; Hum, *Homo sapiens*; Dog, *Canis familiaris*; Mus, *Mus musculus*; Chick, *Gallus gallus*; Fugu, *Fugu rubripes*; Zebra, *Danio rerio*; Rat, *Rattus norvegicus*. Proteins accession numbers: XP__081212 NP__000100 O97592 NP__031894 CM31746__009055 CAA58496. The Fugu sequences are manually corrected GENSCAN predictions from genomic scaffolds ~~(www.igi.doe.gov/fugu, Scaffold 234)~~. The zebrafish utrophin sequence is predicted from the zebrafish genome project. The tree has been made from partial sequences corresponding to the zebrafish protein.

Please replace paragraph [0046] from US 2007/00506054 A1 the publication with the following amended paragraph:

[0046] Sequences were aligned using CLUSTALW (v1.82 with default settings) (Higgins, D. G., Thompson, J. D. & Gibson, T. J. Using CLUSTALW for multiple sequence alignments. *Methods in Enzymology* 266, 383-402 (1996)). Positions in alignments containing gaps were omitted from subsequent analyses. All phylogenetic trees were constructed by the neighbour-joining method (Saitou, N. & Nei, M. The neighbor joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology of Evolution* 4, 406-425 (1987)) based on the proportion of amino acid sites at which sequences compared were different. The reliability of each interior branch of a given topology was assessed using the bootstrap interior branch test with 1000 bootstrap replications (Dopazo, J. Estimating errors and confidence intervals for branch lengths in phylogenetic trees by a bootstrap approach. *Journal of Molecular Evolution* 38, 300-304 (1994)). Phylogenetic trees were constructed using MEGA (Kumar, S., Tamura, K., Kakobsen, I. B. and Nei, M. MEGA2: molecular evolutionary genetics analysis software. *Bioinformatics* 17, 1244-1245 (2001)) ~~(v2.1; http://www.megasoftware.net/)~~ and alignments were examined and formatted

in GeneDoc ~~(v2.6.02;http://www.psc.edu/biomed/genedoc/)~~. The Fugu data has been provided freely by the Fugu Genome Consortium for use in this publication/correspondence only.

Please replace paragraph [0057] from US 2007/00506054 A1 with the following amended paragraph:

[0057] Rooted tree (FIG. 4B) showing dystrophin and utrophin proteins in vertebrates. The tree is rooted using *Drosophila melanogaster* dystrophin. The numbers on each arm represent the percentage of 1000 bootstrap trials that support the branch. DYS, dystrophin; UTRO, utrophin, Hum, *Homo sapiens*; Dog, *Canis familiaris*; Mus, *Mus musculus*; Chick, *Gallus gallus*; Fugu, *Fugu rubripes*; Zebra, *Danio redo*; Rat, *Rattus norvegicus*. Proteins accession numbers: *Drosophila* dystrophin, XP__081212; Human dystrophin, NP__000100; Dog dystrophin, O97592; Mouse dystrophin, NP__031894; Chicken dystrophin, CAA31746, Human utropnin, NP__00955; Mouse utrophin, CAA58496. The Fugu sequence is a manually corrected GENSCAN prediction from a genomic scaffold ~~(www.jgi.doe.gov/fugu, Scaffold 234)~~. The tree has been made from partial sequences corresponding to the zebrafish protein.